MPSRCH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Oct 31 08:33:41 1996: MasPar time 295.79 Seconds
                   1189.730 Million cell updates/sec

Tabular output not generated.

Title: >PCT-US96-14730-5
Description: (1-463) from PCTUS9611730.seq
Perfect Score: 463
N.A. Sequence: 1 CAATACGATATTACCGAATA.........CCGGTGAAAGTAAGCAGSTC 463
Comp: GTTATCGTATAATGCTTAT.........GGCCACTTTCATTCGTCWAG

Scoring table: TABLE default
                Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 270440 seqs, 380027776 bases x 2

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database: embl-new3
   1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN
   9:PRI1 10:PRI2 11:PRO 12:ROD 13:SYN 14:UNC 15:VRT
  16:VIR1 17:VIR2

Database: genbank-new1
  18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7
  25:BCT8 26:BCT9 27:INV1 28:INV2 29:INV3 30:INV4 31:INV5
  32:INV6 33:MAM1 34:MAM2 35:PAT1 36:PAT2 37:PAT3 38:PHG
  39:PLN1 40:PLN2 41:PLN3 42:PLN4 43:PLN5 44:PLN6 45:PLN7
  46:PLN8 47:PRI1 48:PRI2 49:PRI3 50:PRI4 51:PRI5 52:PRI12
  53:PRI7 54:PRI8 55:PRI9 56:PRI10 57:PRI11 58:PRI12
  59:PRI13 60:ROD1 61:ROD2 62:ROD3 63:ROD4 64:ROD5 65:ROD6
  66:ROD7 67:STR 68:SYN 69:UNA 70:UNA 71:VRL1 72:VRL3
  73:VRL4 74:VRL5 75:VRL6 76:VRL7 77:VRT1 78:VRT2 79:VRT3
  80:BCT 81:INV1 82:INV2 83:MAM 84:PHG 85:PLN 86:PRI
  87:ROD 88:STR 89:SYN 90:UNA 91:VRL 92:VRT

Database: u-embl45_92
  93:part1

Statistics: Mean 11.110: Variance 8.217: scale 1.352

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description	Pred. No.
1	c	294	63.5	2884	45	TOMHMG2A	Tomato 3-hydroxy-3-me	3.83e-142
2	c	36	7.8	1095	40	DDICSA	Dictyostelium discoid	2.69e-03
3	c	36	7.8	3700	28	DDGP80G.	D.discoideum gp80 gen	2.69e-03
4		33	7.1	14001	5	PFCOMPIRB	P.falciparum complete	4.75e-02
5		33	7.1	14001	82	PFCOMPIRB	P.falciparum complete	4.75e-02
6		32	6.9	1283	28	DDDD31GE	D.discoideum (AX-4) D	1.21e-01
7		32	6.9	2379	5	DD31	D.discoideum culminat	1.21e-01
8		31	6.7	6615	41	MISDCYTB	S.douglasii gene for	3.03e-01
9		30	6.5	854	46	YSLMTIG08	Yeast (T.glabrata) mi	7.52e-01
10		30	6.5	854	41	MITGTRN6	Torulopsis glabrata m	7.52e-01
11	c	30	6.5	865	31	PLU39369	Parastenopa limata 16	7.52e-01
12	c	30	6.5	1868	76	VSVGLYPQ	vesicular stomatitis	7.52e-01
13		29	6.3	116	35	A08900	H.sapiens (haplotype	1.84e+00
14		29	6.3	300	40	DDIGP24	D.discoideum glycopro	1.84e+00
15	c	29	6.3	3075	32	XPFRNAPOL	P.falciparum gene for	1.84e+00
16		29	6.3	7038	31	PFGP195A	Plasmodium falciparum	1.84e+00
17		29	6.3	8633	31	PFPFMDR1	P.falciparum pfmdr1 g	1.84e+00
18		29	6.3	15421	5	PFCOMPIRA	P.falciparum complete	1.84e+00
19		29	6.3	15421	82	PFCOMPIRA	P.falciparum complete	1.84e+00
20		29	6.3	22243	31	PFAVAR23A	Plasmodium falciparum	1.84e+00
21	c	28	6.0	1860	76	VSVGLYPR	vesicular stomatitis	4.42e+00
22	c	28	6.0	1950	28	DDECMA	D.discoideum ecmA pro	4.42e+00
23	c	28	6.0	2858	46	YSCMTCG18	Saccharomyces cerevis	4.42e+00
24	c	28	6.0	5726	29	DROANTPS2	D.malanogaster positi	4.42e+00
25		28	6.0	14001	82	PFCOMPIRB	P.falciparum complete	4.42e+00
26		28	6.0	14001	5	PFCOMPIRB	P.falciparum complete	4.42e+00
27	c	28	6.0	17084	33	DVMTGNME	D.virginiana mitochon	4.42e+00
28	c	28	6.0	28951	86	HSL161C2	Human DNA sequence fr	4.42e+00
29		28	6.0	28951	10	HSL161C2	Human DNA sequence fr	4.42e+00
30	c	28	6.0	34037	28	CELF43C9	Caenorhabditis elegan	4.42e+00
31		28	6.0	34860	28	CELR173	Caenorhabditis elegan	4.42e+00
32	c	28	6.0	78520	93	MISCCG	S.cerevisiae mitochon	4.42e+00
33	c	27	5.8	525	29	DMSAT02	Drosophila satellite	1.05e+01
34		27	5.8	872	32	TCU39381	Toxotrypana curvicaud	1.05e+01
35	c	27	5.8	1137	39	BJ2SSTP	B.juncea DNA for 2S s	1.05e+01
36	c	27	5.8	1305	40	DICALA	Dictyostelium discoid	1.05e+01
37	c	27	5.8	1722	41	MISC38	Yeast mitochondrial D	1.05e+01
38	c	27	5.8	1861	76	VSVGLYPO	vesicular stomatitis	1.05e+01
39	c	27	5.8	1993	39	BNNAPIN	Brassica napus napB g	1.05e+01
40	c	27	5.8	2160	40	CCRUBISCO	C.caldarium operon of	1.05e+01
41	c	27	5.8	3058	62	MUSHSP25A	Mus musculus small he	1.05e+01
42	c	27	5.8	3289	39	BNANAPA	B.napus napA gene enc	1.05e+01
43	c	27	5.8	7158	42	NGU15605	Nicotiana glutinosa v	1.05e+01
44	c	27	5.8	10213	31	PFU27338	Plasmodium falciparum	1.05e+01
45	c	27	5.8	23016	32	TRBKPGEN	Trypanosoma brucei br	1.05e+01

ALIGNMENTS

RESULT   1
LOCUS   TOMHMG2A   2884 bp   DNA   PLN   14-OCT-1992
DEFINITION   Tomato 3-hydroxy-3-methyl glutaryl coenzyme A reductase (hmg2)
             gene, complete cds.
ACCESSION   M63642
NID   g170451
KEYWORDS   3-hydroxy-3-methylglutaryl coenzyme A reductase.
SOURCE   Lycopersicon esculentum (strain VFNT cherry) DNA.
ORGANISM   Lycopersicon esculentum
             Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida;
             Asteridae; Solanales; Solanaceae.
REFERENCE   1 (sites)
AUTHORS   Yang,Z., Park,H.S., Lacy,G.H. and Cramer,C.L.
TITLE   Differential activation of potato 3-hydroxy-3-methyl glutaryl
             coenzyme A reductase genes by wounding and pathogen challenge
JOURNAL   Plant Cell 3, 397-409 (1991)
MEDLINE   93005707
REFERENCE   2 (sites)
AUTHORS   Park,H.S., Denbow,C.J. and Cramer,C.L.
TITLE   Structure and nucleotide sequence of tomato HMG2 encoding
             3-hydroxy-3-methyl glutaryl coenzyme A reductase
JOURNAL   Plant Mol. Biol. 20, 327-331 (1992)
MEDLINE   93044487
COMMENT   NCBI gi: 170451
FEATURES   Location/Qualifiers
source   1..2884
             /organism="Lycopersicon esculentum"

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exon            /strain="VFNT cherry"
                /sequenced_mol="DNA"
                201..1347
                /gene="hmg2"
                /number=1
CDS             join(311..1347,1430..1611,1813..2159,2575..2817)
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                APMAPPQPSMSMVEKPAPLITSASSGEDEEIIKSVVQGKIPSYSLESKLGDCKRAASI
                MATTEGCLVASTNRGCKAIYASGGATCILLRDGMTRAPCVRFGTAKRAAELKFVEDP
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                LQNEYPDMDVIGISGNFCSDKKPAAVNWIEGRGKSVVCEAIITEEVVKKVLKTEVAAL
                VELMLKNLTGSAMAGALGGFNAHASNIVSAVFIATGQDPAQNIESSHCITMMEAVND
                GKDLHISVTMPSIEVGTVGGGTQLASQSACLNLLGVKGANREAPGSNARLLATVVAGS
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intron          1348..1429
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                /number=1
exon            1430..1611
                /gene="hmg2"
                /number=2
intron          1612..1812
                /gene="hmg2"
                /number=2
exon            1813..2159
                /gene="hmg2"
                /number=3
intron          2160..2574
                /gene="hmg2"
                /number=3
BASE COUNT      829 a    560 c    614 g    881 t
ORIGIN

Query Match             63.5%;  Score 294;  DB 45;  Length 2884;
Best Local Similarity   99.4%;  Pred. No. 3.83e-142;
Matches 306;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  1;

Db    1 taatagcccagttcgtatccaaatatttacactgaccagtcaactgactatataaaa 60
         ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Qy  147 TAATAGCCCAGTTCGTATCCAAATATTTACACTGACCAGTCAACTTGACTATATAAAA 206

Db   61 cttcacttcaaaaaattaaaaagaaaagaaaaagtatatattgtaaaagataactccat 120
         |||| |||||||||||||||||||||||||||||| |||||| ||||||| | ||||||
Qy  207 CTTTACTTCAAAAAATTAAAAAAAAAAAAAAAAAGAAAAGTATATTATTGTAAAAGTAATACTCCAT 266

Db  121 tcaaaatataaatgaaaaagtccagcgcggcaaccgggtcctataaatacattc 180
         ||||||||||||||||||||||||| ||||||||||||||  ||||||||||||
Qy  267 TCAAAATATAAAATGAAAAAGTCCAGCGGCGGCAACCGGGTTCCT--ATAAATACATTTC 324

Db  181 ctacatctctctcctcccacatccatcactccttctttaacaattatacttgtcaat 240
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Qy  325 CTACATCTTCTCTTCTCCTCACATCCCATCACTCACTTCTTTTAACAATTATTACTTGTCAAT 384

Db  241 catcaatcccacaacaacacttttctctccctctttttcctcaccggcgcagaacttac 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  385 CATCAATCCCACAAACAACACTTTTTCTCTCCCTCTTTTTTCCTCACCGGCGGCAGAACTTAC 444

Db  301 cggtqaaa 308
         |||||||
Qy  445 CGGTGAAA 452

RESULT  2
LOCUS       DDICSA      1095 bp    DNA             PLN       16-JUL-1992
DEFINITION  Dictyostelium discoideum cAMP-regulated promoter (csA) gene,
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ACCESSION   M87525
NID         g167697
KEYWORDS    cAMP-regulated promoter; cell adhesion molecule.
SOURCE      Dictyostelium discoideum (strain AX2) early development DNA.
ORGANISM    Dictyostelium discoideum
            Eukaryota; Fungi; Myxomycota; Acrasiomycetes; Dictyosteliales;
            Dictyosteliaceae.
REFERENCE   1 (bases 1 to 1095)
AUTHORS     Faix,J., Gerisch,G. and Noegel,A.A.
TITLE       Overexpression of the CSA cell adhesion molecule under its own
            camp-regulated promoter impairs morphogenesis in dictyostelium
JOURNAL     J. Cell Sci. 102, 203-214 (1992)
MEDLINE     93016323
COMMENT     NCBI gi: 167697
FEATURES             Location/Qualifiers
     source          1..1095
                     /organism="Dictyostelium discoideum"
                     /strain="AX2"
                     /dev_stage="early development"
                     /sequenced_mol="DNA"
     TATA_signal     884..890
                     /gene="csa"
     mRNA            905..1095
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                     /partial
     CDS             1084..1095
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                     /codon_start=1
BASE COUNT      518 a     69 c     95 g    413 t
ORIGIN

Query Match             7.8%;   Score 36;  DB 40;  Length 1095;
Best Local Similarity   71.1%;  Pred. No. 2.69e-03;
Matches 69;  Conservative  0;  Mismatches 27;  Indels  1;  Gaps  1;

Db  835 acttttttttttttttttttttttttttttttttattatttttttttattatttctt 894
         ||||||| ||||  |  | |  ||||||| || | |||||| ||| |  ||||||||
Cp  289 ACTTTTTCATTTATATTTGAATGAGAATATTTTGAAGGAGTATTATCTTTTACAATAATATACT-TTCTTT 231

Db  895 ttttttttttttaaattaaaaatttttataaattca 931
         |||||||| ||||  |  | |||||||||||||||||
Cp  230 TTTTTAATTTTTGAAGTAAAGTTTTATATAGTCA 194

RESULT  3
LOCUS       DDGP80G     3700 bp    DNA             INV       21-JUL-1993
DEFINITION  D.discoideum gp80 gene.
ACCESSION   X66483 S45379
NID         g7289
KEYWORDS    cell adhesion molecule; gp80 gene.
SOURCE      slime mold.
ORGANISM    Dictyostelium discoideum
            Eukaryotae: mitochondrial eukaryotes; Dictyostelida;
            Dictyostelium.
REFERENCE   1 (bases 1 to 3700)
AUTHORS     Siu Besst Inse.C.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1992) to the EMBL/GenBank/DDBJ databases. C. Siu
            Besst Inse, 112 College St. Rm. 207, Toronto, Ontario, Canada M5G
            1L6, CANADA
REFERENCE   2 (bases 1 to 3700)
AUTHORS     Desbarats.L., Lam.T.Y., Wong.L.M. and Siu,C.H.
TITLE       Identification of a unique cAMP-response element in the gene
            encoding the cell adhesion molecule gp80 in Dictyostelium
            discoideum
JOURNAL     J. Biol. Chem. 267 (27), 19655-19664 (1992)
MEDLINE     92406924
COMMENT     NCBI gi: 7289
FEATURES             Location/Qualifiers
     source          1..3700
                     /organism="Dictyostelium discoideum"
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